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Evaluation of a Visual Census Method for Reef Fishes at Tektite Reef, Virgin Islands National Park, St. John, U.S. Virgin Islands: Determination of Optimal Sample Size

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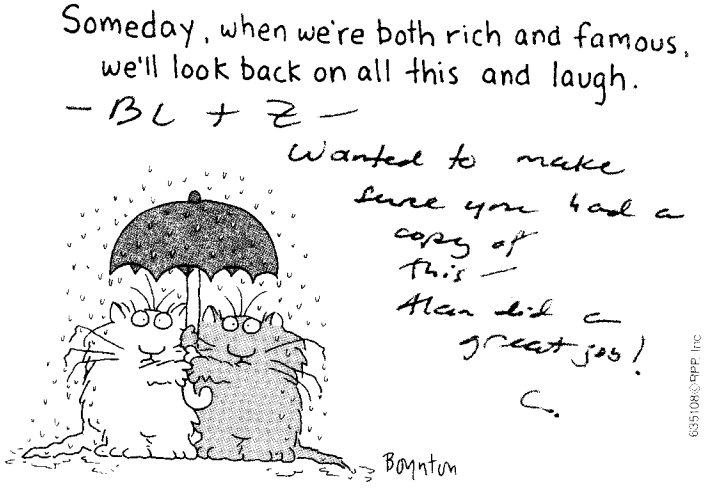

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ABSTRACT

During investigations conducted since 1984, a random point visual census technique for fishes has been used in Virgin Islands National Park. An "over sampling" effort of the reef fishes at Tektite Reef was conducted from 9 to 11 July 1999 to determine the optimal sample size for point counts conducted on that reef. A total of 58 visual point counts was conducted on edge (n=13) and platform habitats (n=45) and compared to our typical haphazard sample of 18 censuses. Our typical sample size of 18 censuses at Tektite Reef appears adequate to detect changes in number of species and number of individuals for the entire assemblage and for many trophic guilds at a 20% level. Continued stratification by edge and platform microhabitats seems appropriate based on differences in biomass and detrended correspondence analysis results for assemblage structure. Despite high coefficients of variation for some parameters and guilds, our current sampling protocol for Tektite Reef can detect an ongoing decline of 5% in nine years. Increasing alpha levels to 0.20 would improve the ability to detect these changes and is consistent with the precautionary approach to management. For number of species, number of individuals, and biomass there were no significant differences between values obtained using random vs. haphazard sampling. From these results, continues haphazard sampling appears to be preferable to random sampling due to the time and cost involved in the latter sampling design. This study was conducted in order to evaluate the validity/accuracy of prior data collections at Tektite Reef and determine the optimal sample size for future work at this site. It is also meant to serve as a framework to develop an optimal sampling protocol for the National Park Service for the island of St. John and other locations to evaluate coral reef fisheries resources. In order to address the issue of number of sites and number of samples at a broader spatial scale, a more intensive sampling effort will need to be conducted on other reefs and at a variety of reef types.

INTRODUCTION

Coral reef fishes have been selected as an important community component for monitoring in Virgin Islands National Park (VIIS). This will allow documentation of their status and change over time for the purpose of better understanding how natural and anthropogenic factors influence fish assemblages. This information is imperative for the effective management of these resources. Quantitative sampling of reef fishes in Virgin Islands National Park has been conducted since the mid 1980's with annual monitoring being conducted since 1988 (Beets 1993). The long-term data on fish populations in VIIS is unprecedented in duration and area of coverage for the Caribbean and a strong need exists to continue and enhance this program. The aims of this study are to evaluate the validity/accuracy of prior data collections at Tektite Reef, VIIS and determine the optimal sample size for future work at this site. It is also meant to serve as a framework to develop an optimal sampling protocol for the National Park Service for the island of St. John and other locations to evaluate coral reef fisheries resources. One of the specific issues that are addressed in this study is the concern of haphazard vs. random sampling to assess coral reef fishes.

During investigations conducted over many years, a random point visual census technique for fishes has been used in Virgin Islands National Park. This technique, described by Bohnsack and Bannerot (1986), has been used with modifications throughout the Caribbean. The basic technique is conducted by a diver settling on the reef substrate at a haphazardly selected point. If the surrounding area is greater than 50% hard substrate and/or reef, then the area is briefly described in terms of substrate type, estimated coral cover, dominant benthic organisms, relative topographic complexity, depth and location on the reef. If the area is greater than 50% sand, the diver moves to another point on the reef. All fish species observed are listed within a 7.5 m radius cylinder for 5 min. Numbers and sizes of fishes of each species (in separate size classes) are added following the 5 min listing period. Live wet weight (W) was calculated from the visually estimated mean fork length (FL) for each size class for each species using the relation $W = a(FL)^b$. Values of the fitting parameters a and b for each species were derived from Bohnsack et al. (1986) and the FishBase web site (http://fishbase.org/). Biomass of all fishes recorded in all censuses was obtained by multiplying the mean live wet weight for each size class for each species by the total number of individuals observed in that size class.

Rafe Boulon and others first used the random point count technique in Virgin Islands National Park in the 1980's (Boulon 1987). Joe Kimmel and Jim Tilmant modified this technique to survey Dry Tortugas National Park in 1987 (Kimmel 1992) and Virgin Islands National Park during 1989-1994. Their modification used a 5-m radius cylinder and 15 min time interval with the last 5 min of the 15 min total used to search and enumerate species and individuals throughout the cylinder. The unmodified technique was intensively used at four sites within Virgin Islands National Park from 1988 to 1991 and four to fourteen sites surveyed annually from 1995 through 1999. Starting in 1995, the unmodified technique has been used during the annual fish sampling within Virgin Islands National Park. The change back to the unmodified technique in 1995 from previous modifications was to standardize the technique with investigators working elsewhere in the Caribbean (esp. Jim Bohnsack working in the Florida Keys National Marine Sanctuary and Dry Tortugas National Park).

Four reefs (Yawzi Point Reef, Tektite Reef, Newfound Bay, and Haulover Bay) have been sampled annually for reef fish using visual point counts over a ten-year period. Fourteen additional reefs have been monitored several times during this time. During this period 3-4 major storms have affected fish assemblages on St. John reefs. Two reef sites (Yawzi Point Reef and Cocoloba Cay Reef) were intensively monitored over a two year period (1988-90) on a monthly basis to document seasonal variation (Beets and Friedlander 1990, Beets 1993). We have stratified our sampling to include only the two subhabitats (platform and edge) of the lower forereef zone. This habitat is the dominant reef habitat (excluding gorgonian-dominated habitat) around St. John. This habitat is spatially complex with high coral cover and has the greatest species richness and numerical abundance of fishes. Normally, sampling was conducted from the reef-sand interface to the middle portion of the reef platform which was usually the lower forereef dominated by *Montastrea annularis*. Over the years, sample size per site varied depending on the availability of time, money, and resources.

Site description and survey methodology

Tektite Reef has been monitored for fishes using visual point counts since 1989. It is located near Cabritte Horn Point, in Lameshur Bay on the south side of St. John. The reef rises 1.5 to 5 m above the adjacent sea floor, with high coral cover dominated by *Montastrea annularis*. Linear grooves or channels that are partly filled by carbonate sand are orientated in a NE/SW direction across the reef (Clifton and Phillips 1972). Tektite Reef had the highest species richness, greatest number of individuals, and second greatest biomass of fish for all reefs sampled around St. John from 1989 to 1994 (Beets and Friedlander, unpublished data).

An "over sampling" effort of the reef fishes at Tektite Reef was conducted from 9 to 11 July 1999 to determine the optimal sample size for point counts conducted on that reef. This study was conducted in order to evaluate the validity/accuracy of prior data collections at Tektite Reef and determine the optimal sample size for future work at this site. It is also meant to serve as a framework to develop an optimal sampling protocol for the National Park Service for the island of St. John and other locations to evaluate coral reef fisheries resources. Ten fiberglass transects lines were laid out roughly parallel to the reef edge (Fig. 1). Along each line, point counts were conducted at 15-m intervals. A total of 58 visual point counts were conducted on edge (n=13) and platform habitats (n=45). Desert Star's Aqua Map system, an underwater survey and navigation product that uses sonar triangulation within an acoustical array to map features and locate points was used to delineate the area of the reef and estimate total areal coverage. Based on the Aquamap system, the total areal coverage of Tektite Reef was ca. 13,500 m^2. Samples were limited to coral habitat (excluding bedrock, rubble, cobble, and sand zones), that has over 50% carbonate hard-bottom substrate within 15m cylindrical samples. The 58 censuses (15-m diameter) had a total coverage of 10,250 m^2 or roughly 76% of the total area. Considering the amount of sand and marginal reef habitat, we are confident that the 58 censuses sampled nearly the entire coral reef habitat of the reef. Data from the "oversampling" effort were compared to a subset of 18 haphazardly selected censuses from these data to evaluate the two methods and to determine optimal sample size (number of point counts).

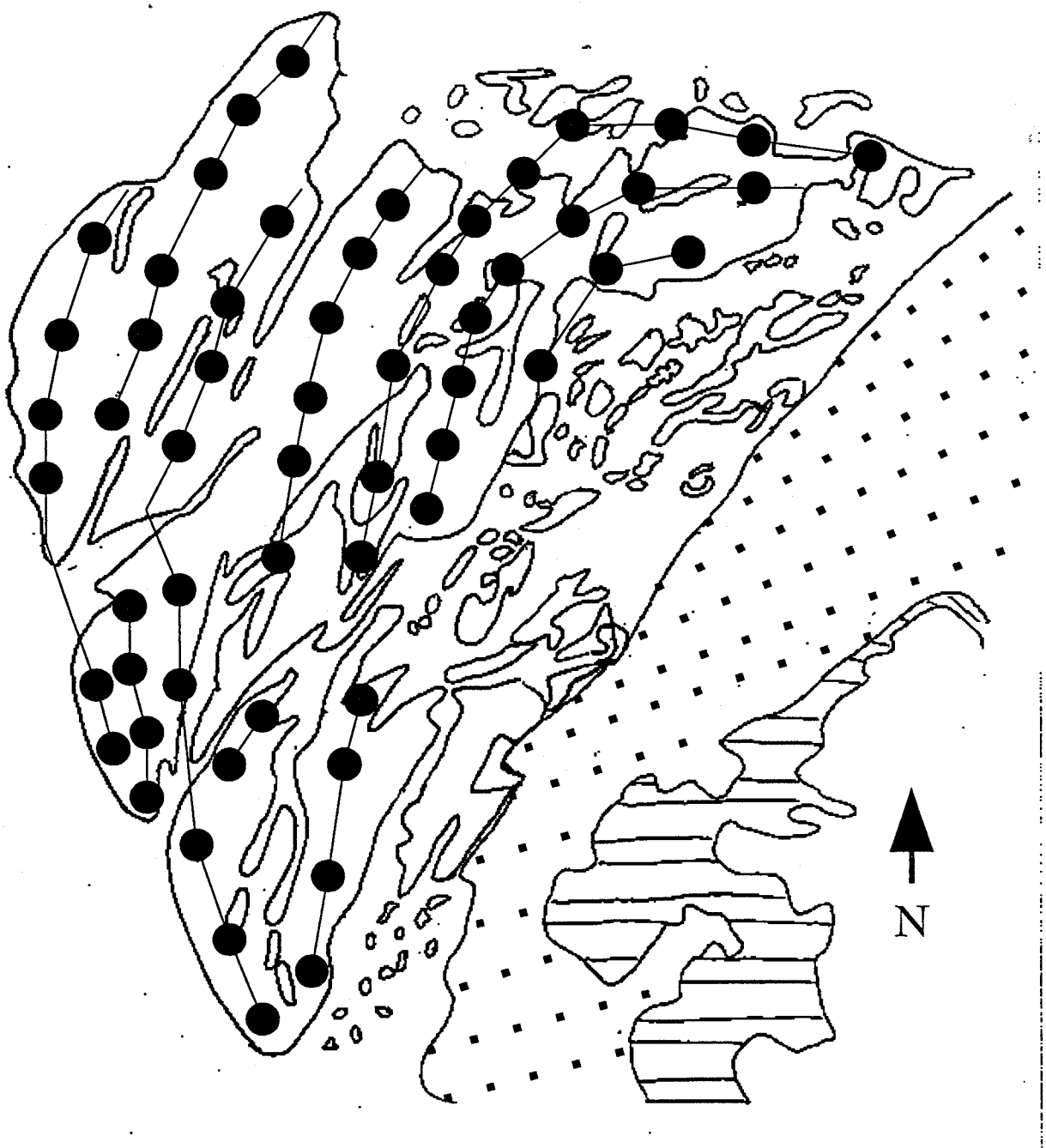

Figure 1. Locations of visual point counts conducted on Tektite Reef, St. John, 9-11 July 1999. Dotted lines denote areas of bedrock gravel. Solid horizontal lines denote bedrock outcrops. Total number of censuses is 58.

RESULTS

Sample size optimization analysis

A species cumulation curve was used to examine the relationship between the cumulative number of species and number of samples at Tektite Reef (Fig. 2). The cumulative number of species reached an asymptote at 22 samples. Our usual size of 18 censuses accounted for 96% of the total number of species observed at Tektite Reef during the sampling effort.

A technique developed by Bros and Cowell (1987) using the standard error of the mean to resolve statistical power was used to determine the number of samples needed based on number of species, number of individuals, and biomass. This method uses a Monte Carlo simulation procedure to generate a range of sample sizes versus power. The sample size at which a further increase in sample size does not substantially increase power (decreasing SEM) is taken as the minimum suitable number of samples. A Lotus macro program written by Doug Harper of the NMFS/SEFSC/Miami Laboratory was used to conduct this analysis. For number of species and number of individuals, high and low standard error of the mean begin to level off and converge at ca. 11-13 samples (Fig. 3). Biomass shows a much higher degree of variability and does not level off and converge until 15 to 20 samples. All analysis for number of individuals and biomass excluded masked gobies (*Coryphopterus personatus)* because they were ubiquitous and their large numbers (1000's) masked trends in the remainder of the fish assemblage.

The relationship of sample size with accuracy of the mean was examined for number of species, number of individuals, and biomass from the 58 censuses conducted at Tektite Reef. Sample means were compared to a theoretical population mean using the t-distribution:

$$t - value = \frac{\text{sample mean} - \text{population mean}}{\sqrt{\text{sample variance} / \text{sample size}}}$$

(Eckblad 1991). The equation was solved for sample size using various values of accuracy (accuracy = [sample mean - population mean]/sample mean). Using a Type I error rate of 0.10, the number of samples needed to detect changes in assemblage characteristic decreases rapidly with relatively slight losses in accuracy. A Type I error rate of 0.10 was chosen over the traditional 0.05 because failing to detect a change when one is actually occurring (Type II error) could result in a failure to take steps to prevent population collapse. This is the precautionary approach to management as mandated by the Magnuson-Stevens Fishery Conservation and Management Act

The estimated number of samples needed to detect various levels of change varied greatly among the three parameters (mean abundance of species, individuals, and biomass). Figure 4 provides estimates of the number of samples needed to detect various levels of change in the mean abundance of species, individuals, and biomass. Using a Type I error rate of 0.10, the number of samples needed to detect changes decreases rapidly with only a slight decline in accuracy. Less than two samples are required to detect a 20% change in number of species per census while 12.8 censuses are required to detect a 20% change in number of individuals. Again, biomass is highly variable with ca. 140 samples needed to detect a 20% change. Using a Type I error rate of 0. 20 substantially decreases the number of samples needed to detect change

in the 10% to 20% range of accuracy. Less than two samples are required to detect a 15% change in number of species per census while 7.7 censuses are required to detect a 20% change in number of individuals. Again, biomass is highly variable with 84 samples needed to detect a 20% change.

Sample power by trophic guild was extremely variable among different guilds and among different assemblage characteristics (Figure 5). Herbivores and mobile invertebrate feeders showed the least variability and thus changes in number of individuals and biomass could be more easily detected. The mobile invertebrate/piscivore feeding guild was excluded from the figure of number of individuals due to the number of samples required to detect a population change of 20% (506). Mobile invertebrate feeders/piscivores and piscivores were excluded from the biomass figure for the same reasons. A total of 542 samples were required to detect a 20% change in biomass for the mobile invertebrate/piscivore feeding guild, while 2036 samples would be required to detect a 20% change in biomass for piscivores.

Comparison of sampling effort

Assemblage characteristics were compared between the large sampling effort of 58 censuses and our typical sample size of 18 haphazard samples that were a subset of the 58 censuses. There was no significant difference in mean number of species, number of individuals, or biomass between the large sample size and our typical sample size (Table 1).

Since biomass was significantly different between edge and platform habitats (see section below on Edge/platform comparisons), assemblage characteristics for the two sample sizes were compared within each habitat. For both edge and platform habitats, there was no significant difference in mean number of species, number of individuals, or biomass between the large sample size and our typical sample size (Table 2 & 3).

Table 1. Comparison of assemblage characteristics for large sampling effort (n = 58) vs. typical number of samples conducted at Tektite reef (n = 18). Results of Mann-Whitney Rank Sum Test = T. Table values are means for all data pooled with standard deviations in parentheses.

Assemblage characteristic	Large sample (n = 58)	Typical sample (n = 18)	T	P
No. of species	26.9 (3.8)	26.4 (3.6)	662.5	0.714
No. of individuals	268.2 (114.9)	280.7 (123.6)	717.5	0.769
Biomass (g)	9412.0 (13349.6)	15294.3 (21940.7)	767.0	0.369

Table 2. Comparison of assemblage characteristics along edge habitat for large sampling effort (n = 13) vs. typical number of samples conducted at Tektite reef (n = 9). Results of Mann-Whitney Rank Sum Test = T. Table values are means with standard deviations in parentheses.

Assemblage characteristic	Large sample (n = 13)	Typical sample (n = 9)	T	P
No. of species	27.8 (3.0)	28.2 (3.0)	107.5	0.815
No. of individuals	285.8 (94.0)	286.3 (104.7)	103.0	1.000
Biomass (g)	19662.2 (24467.9)	24945.5 (28140.5)	112.5	0.570

Table 3. Comparison of assemblage characteristics in platform habitat for large sampling effort (n = 45) vs. typical number of samples conducted at Tektite reef (n = 9). Results of Mann-Whitney Rank Sum Test = T. Table values are means with standard deviations in parentheses.

Assemblage characteristic	Large sample (n = 45)	Typical sample (n = 9)	T	P
No. of species	26.6 (4.0)	24.7 (3.4)	188.8	0.171
No. of individuals	263.2 (120.7)	275.1 (146.4)	243.0	0.926
Biomass (g)	6450.9 (5251.4)	5643.1 (4636.0)	219.5	0.523

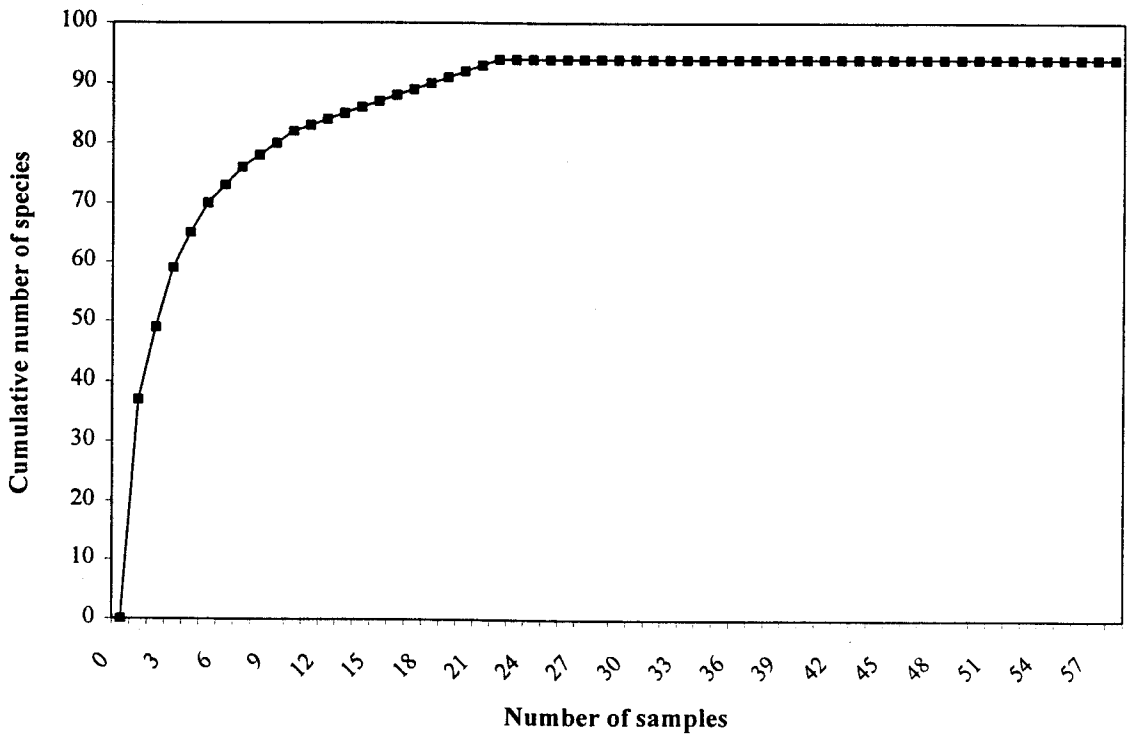

Figure 2. Cumulation curve showing the relationship between the cumulative number of species and the number of samples at Tektite Reef.

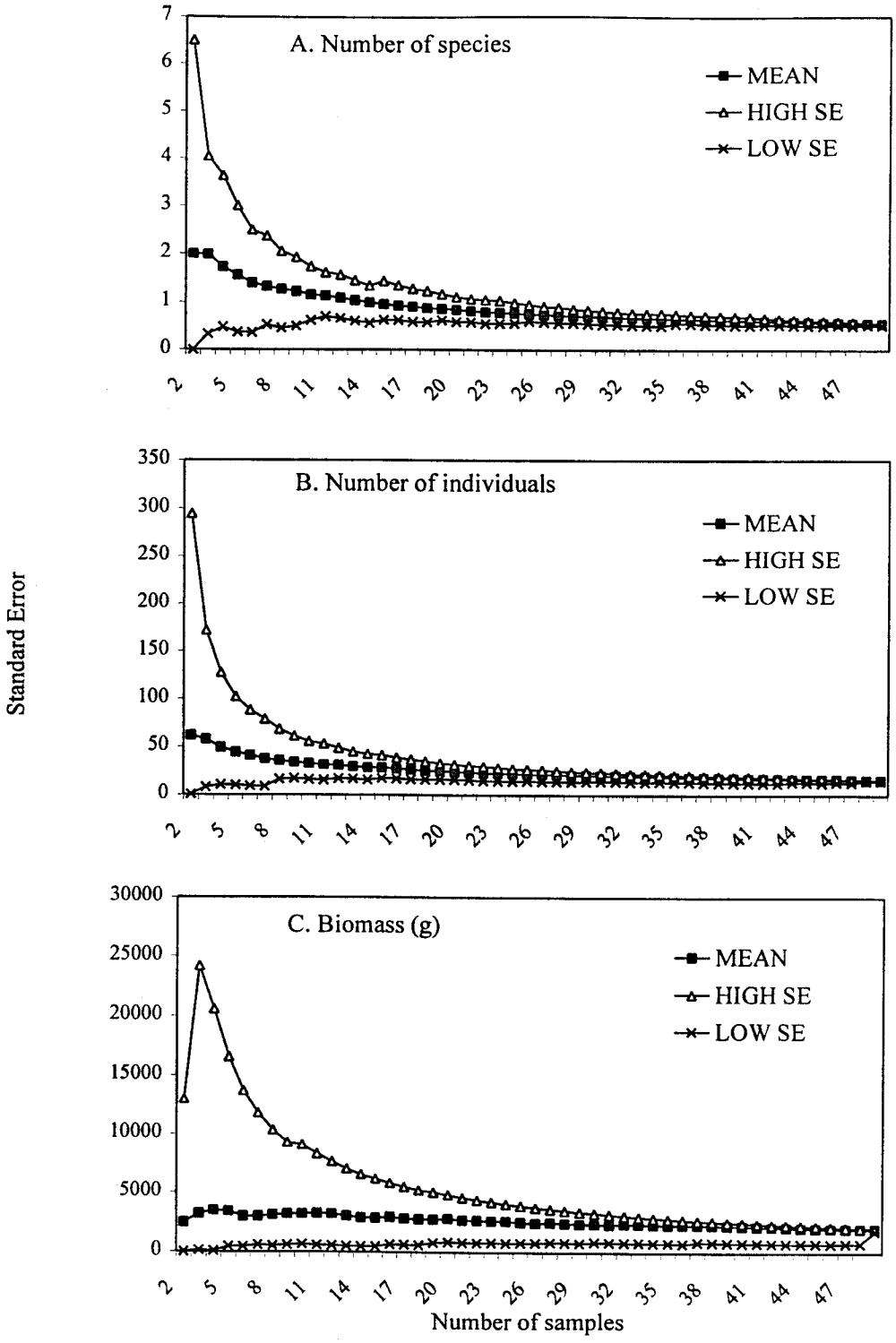

Figure 3. Sample size optimization for number of species, number of individuals, and biomass. Relationship between standard error of the mean (SEM) and sample size at Tektite Reef. Monte Carlo simulation procedure for sample size optimization described by Bros and Cowell (1987).

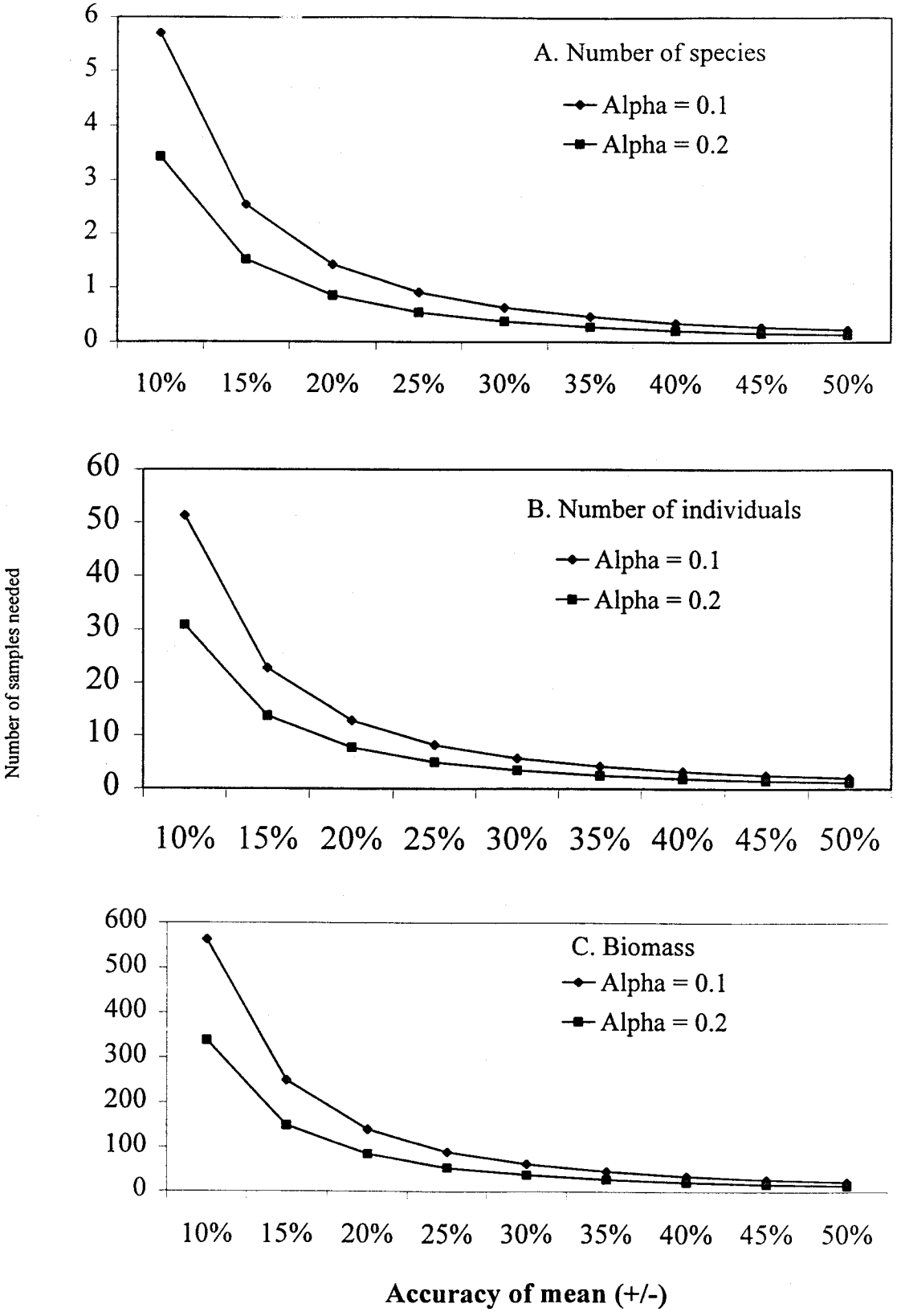

Figure 4. Estimated number of samples needed to detect changes in the mean A. number of species, B. number of individuals, and C. biomass. N = 58, α = 0.10 and 0.20.

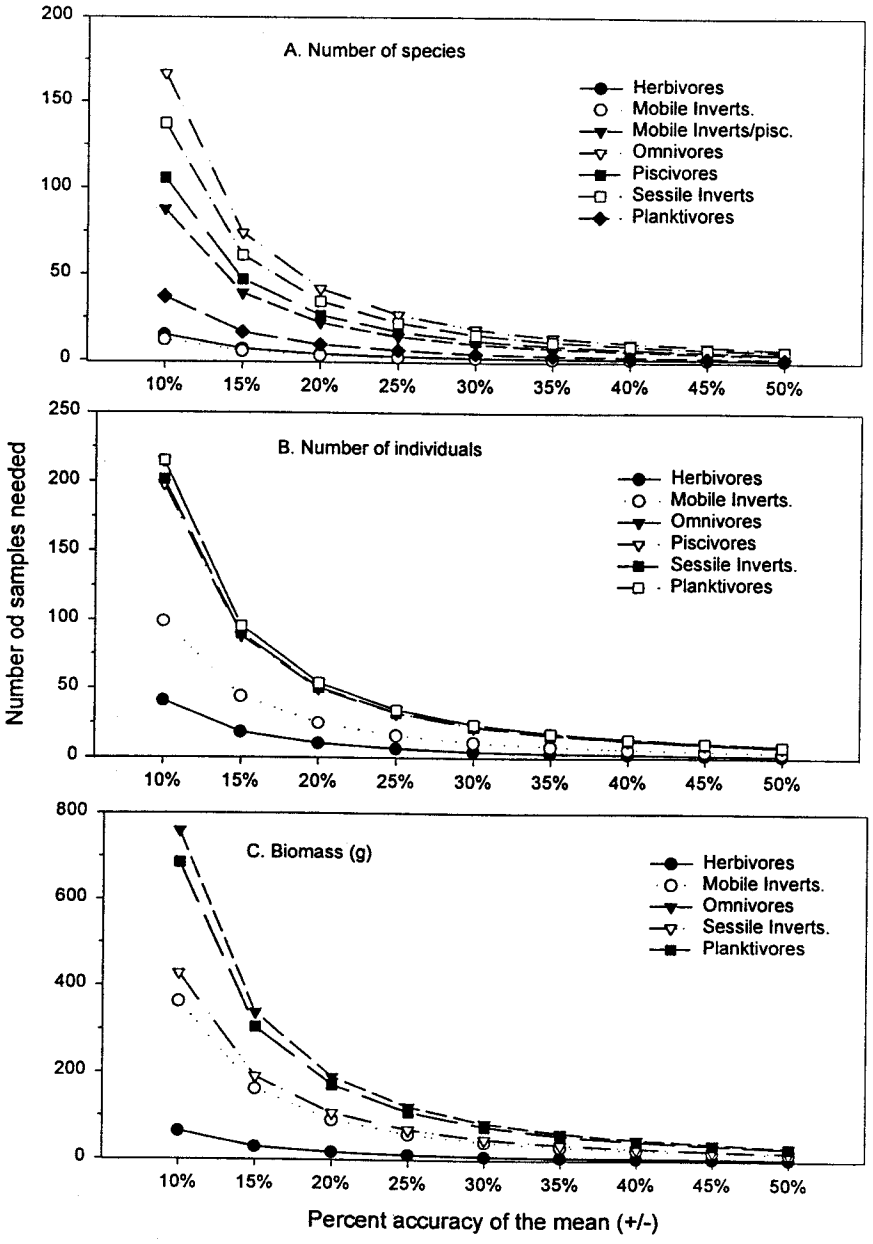

Figure 5. Number of samples required to detect changes in mean assemblage characteristics for various trophic groups. A. Number of species, B. Number of individuals, C. Biomass (g). Alpha = 0.10. Mobile invertebrate/piscivore feeders excluded from B. and C. due to scale. Piscivores excluded from C. due to scale.

Random vs. haphazard sampling

We compared our typical haphazard sample of 18 censuses at Tektite from the larger data set to a random subset of 18 censuses selected from the overall large sampling effort (n = 58). For number of species, number of individuals, and biomass there were no significant differences between values obtained using random vs. haphazard sampling (Table 4).

Table 4. Comparison of assemblage characteristics for 18 random samples vs. our typical haphazard sample of 18 censuses. Results of t-test = t. Table values are means with standard deviations in parentheses. Biomass was ln(x+1) transformed for analysis.

Assemblage characteristic	Random sample (n = 18)	Typical sample (n = 18)	t	P
No. of species	27.2 (3.2)	26.4 (3.6)	0.682	0.500
No. of individuals	266.0 (111.8)	280.7 (123.6)	0.375	0.710
Biomass (g)	14105.5 (22231.8)	15294.3 (21940.7)	0.438	0.664

Assemblage comparisons

Detrended correspondence analysis (DCA), with rare species downweighted, showed a modest degree of overlap in assemblage structure between edge and platform habitats for number of individuals (Figure 6). Assemblage structure based on biomass, and to a lesser degree numerical abundance, showed some separation between the two habitat types (Fig. 6 & 7).

Observer variation

Although observers conducted censuses in different microhabitats, the assemblage structure among observers does not appear to be appreciably different (Figure 8). A Two Way ANOVA was conducted with habitat (edge and platform) and observers (AF, JB, and JM) as fixed factors in the ANOVA. Biomass was ln(x+1) transformed. An unbalanced sample design precluded analysis of interaction terms.

For number of species, a Two Way ANOVA with both factors fixed showed no significant difference between habitats but a significant difference among observers was observed (Table 5). Mean species counts per census were significantly greater for AF compared to JB and JM ($P < 0.05$). The power for the 2 way Model I ANOVA was calculated using eq. 12.43 in Zar (1999). Power is very low for detecting differences in habitat but extremely high for observer differences. This is primarily due to the ratio of the Mean Squares for each factor compared to the Residual or Error Mean Square. Therefore, you are almost guaranteed of committing a Type II error (>99%) in trying to detect a difference in habitats. Number of species per census was not significantly different between JB and JM ($P > 0.05$). One of the reasons for this difference is probably that observers sample different microhabitats while the other reason may be the inclusion or exclusion of small cryptic benthic species (e.g. gobies and blennies) by certain observers.

For number of individuals, a Two Way ANOVA showed no significant difference between habitats or among observers (Table 6). Mean biomass estimates were not significantly different among observers ($P > 0.5$) but were significantly higher on the edge compared to the platform habitat ($P < 0.05$; Table 7).

Table 5. Two way ANOVA for number of species. Habitats are edge and platform. Observers are AF, JB, and JM. Values below observer initials are mean number per census with one standard deviation of the mean in parentheses. All Pairwise Multiple Comparison Procedures (Bonferroni t-test). Underlined means are not significantly different at $\alpha = 0.05$.

Source of variation	DF	SS	MS	F	P	Power
Habitat	1	4.573	4.573	0.601	0.442	0.00
Observer	2	415.3	207.6	27.3	<0.001	>0.99
Residual	54	411.0	7.6			
Total	57	841.4	14.8			

AF	JB	JM
30.5 (2.7)	26.2 (2.5)	23.9 (3.0)

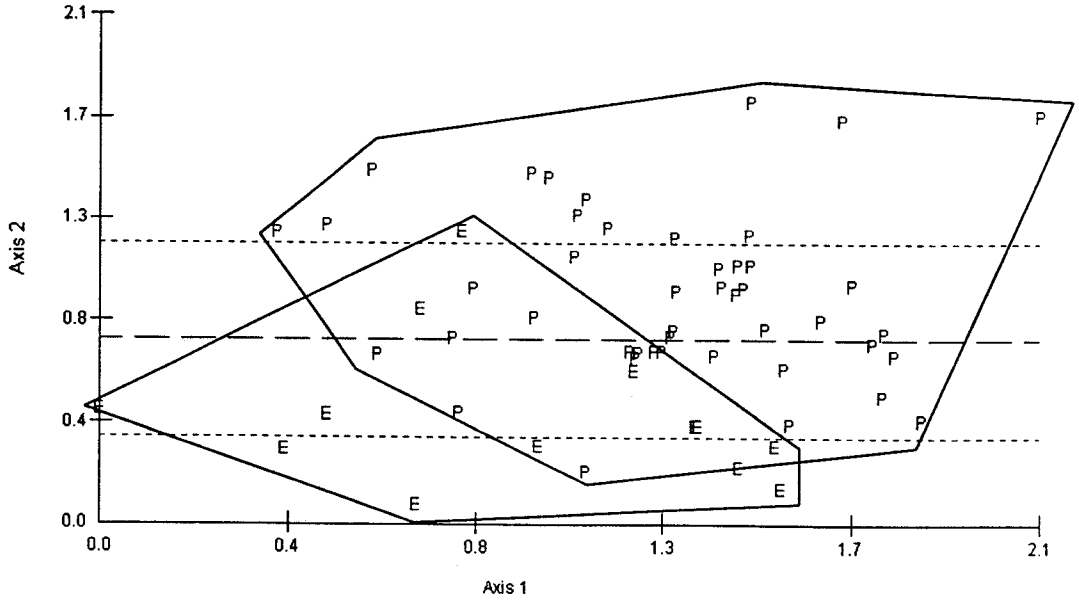

Figure 6. Detrended Correspondence Analysis for Tektite Reef based on numerical abundance. E = edge censuses, P = platform censuses. Long dashed line represents mean eigenvalue. Small dashed lines are 95% confidence intervals.

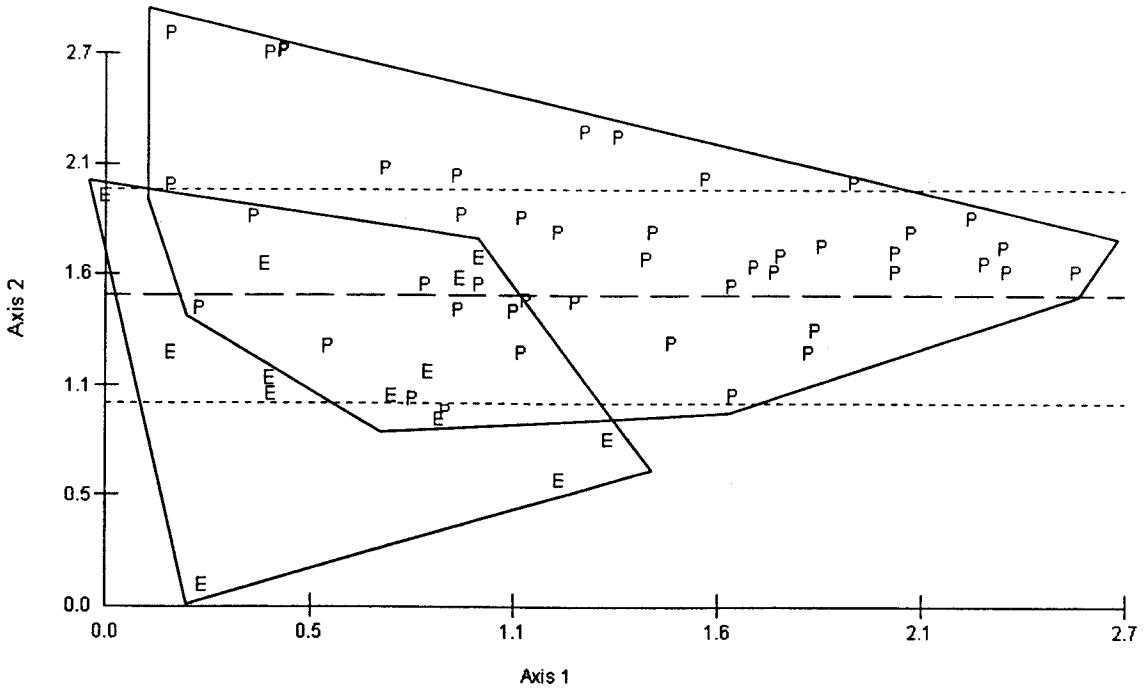

Figure 7. Detrended Correspondence Analysis for Tektite Reef based on biomass.
E = edge censuses, P = platform censuses. Long dashed line represents mean eigenvalue. Small dashed lines are 95% confidence intervals.

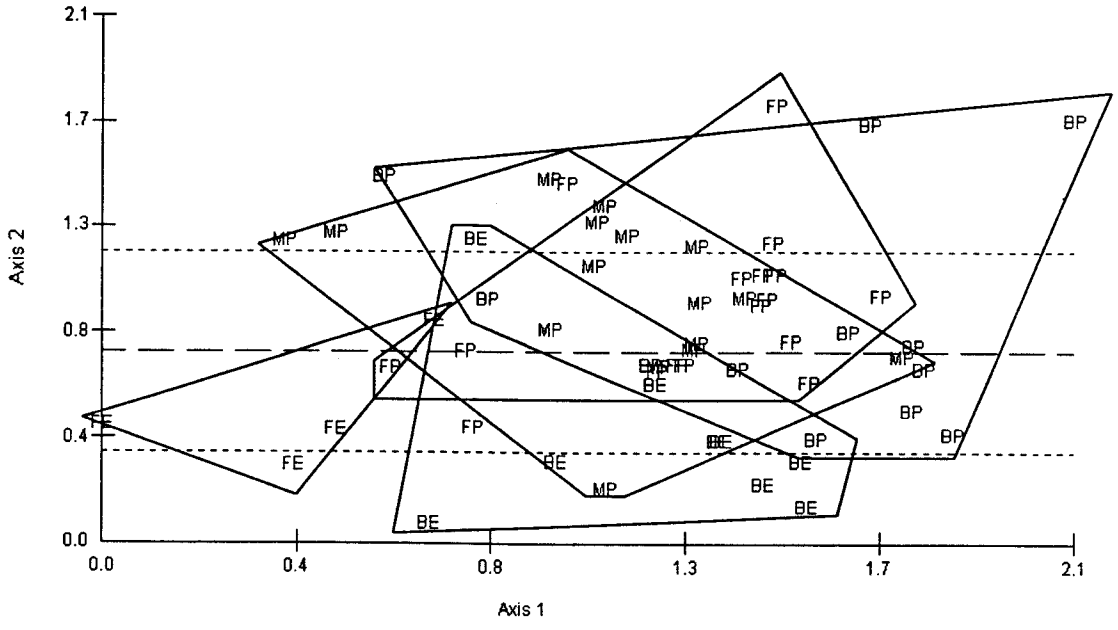

Figure 8. Detrended Correspondence Analysis for Tektite Reef based on numerical abundance Comparison of observers. FE = AF edge, FP = AF platform, BF = JB edge, BP = JB platform, MF = JM edge, MP = JM platform. Long dashed line represents mean eigenvalue. Small dashed lines are 95% confidence intervals.

Table 6. Two way ANOVA for number of individuals. Habitats are edge and platform. Observers are AF, JB, and JM.

Source of variation	DF	SS	MS	F	P	Power
Habitat	1	3432.9	3432.9	0.248	0.620	0.00
Observer	2	303.6	151.8	0.0110	0.989	0.00
Residual	54	747190.0	13836.9			
Total	57	752686.6	13205.0			

Table 7. Two way ANOVA for biomass. Habitats are edge and platform. Observers are AF, JB, and JM. Data were ln(x+1) transformed for analysis. Mean edge biomass = 19662.2 (24467.9); mean platform biomass = 6450.9 (5251.4).

Source of variation	DF	SS	MS	F	P	Power
Habitat	1	7.190	7.190	14.138	<0.001	0.94
Observer	2	1.486	0.743	1.461	0.241	0.12
Residual	54	27.463	0.509			
Total	57	36.618	0.642			

Power analysis of monitoring programs

The information that follows is taken from the USGS web site on power analysis and monitoring programs (http://www.im.nbs.gov/powcase/powcase.html). "Sensitivity of trend detection (effect size) is a good example of a variable often driven by management objectives. What constitutes a "biologically significant" rate of population change? Values seen in the literature tend to range between 3-5% (declines in particular) per year, which translate into 26–40% over 10 years. The stronger the trend, the less effort it takes to detect". The graph below was generated using output of the freeware program *MONITOR* from the USGS (Fig. 9). The figure depicts the minimum number of counts per year required to obtain at least 90% power to detect a population decline of 5% at one site. For example, using 22 samples per year, a parameter with a 25% annual coefficient of variation (CV) could detect a decline of 5% at one site in 5 years.

Coefficient of Variation (COV) data for total assemblage characteristics and characteristics for various trophic guilds are provided in Table 8. In many cases, declines of 5% per year could be detected over a 10-year period. Appendix I lists all fish species (n = 94) observed during the large sampling effort (n = 58) at Tektite Reef. Coefficient of Variation ranged from 46% (number of individuals) and 63% (weight) for the threespot damselfish (*Stegastes planifrons)* to greater than 700% for a number of species that are infrequently encountered at Tektite. Families with low COVs included damselfishes, parrotfishes, and wrasses. Several large snappers (schoolmaster snapper (*Lutjanus analis)* and dog snapper (*L. joco*)), a couple of groupers (coney (*Epinephelus fulvus)* and rock hind (*E. adscensionis)*), and species infrequently encountered at Tektite such as the slender filefish (*Monacanthus tuckeri)*,

balloonfish (*Diodon holocanthus)*, and sergeant major (*Abudefduf saxatilis)* all had very high COVs.

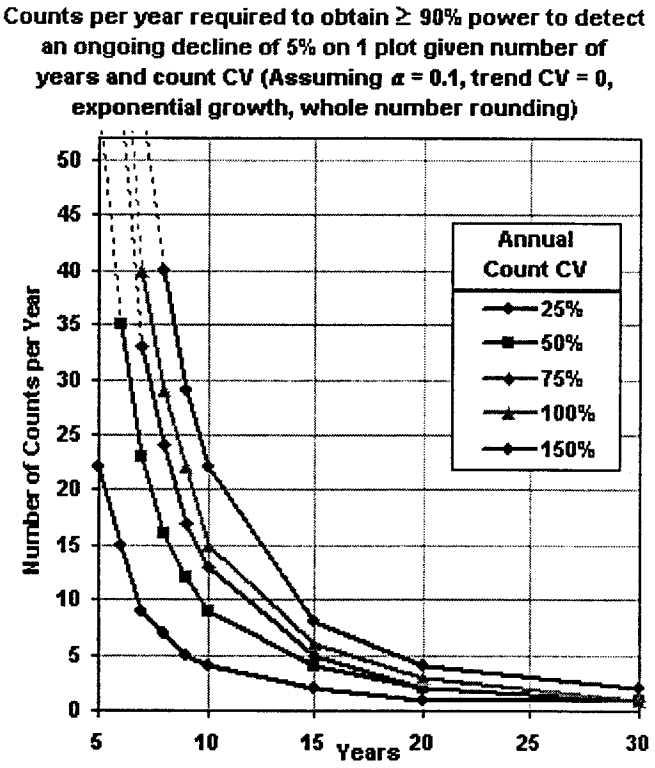

Figure 9. Counts per year required to obtain greater than or equal to 90% power to detect an ongoing decline of 5% on 1 plot given number of years and count CV.

Table 8. Coefficient of Variation (COV) data for total assemblage characteristics and characteristics for various trophic guilds.

Guild	No. Species	No. individuals	Biomass
Entire assemblage	0.14	0.43	1.42
Herbivores	0.23	0.38	0.48
Mobile Inverts.	0.21	0.59	1.14
Mobile inverts./piscivores	0.56	2.69	2.79
Omnivores	0.77	0.88	1.65
Piscivores	0.61	0.91	5.40
Sessile inverts.	0.70	0.84	1.24
Planktivores	0.36	0.85	1.57

Edge/platform comparisons

Of the total of 58 censuses conducted at Tektite Reef from 9 to 11 July 1999, 13 censuses were conducted along edge habitats and 45 in the platform habitat. No significant differences were found for number of species (P = 0.259) or number of individuals (P = 0.236) between the two habitat types (Table 9). Mean census biomass was significantly higher (P = 0.002) on the edge compared to the platform habitats sampled.

Table 9. Comparison of fish assemblage characteristics for large sampling effort conducted at Tektite Reef. Results of Mann-Whitney Rank Sum Test = T. Table values are means with standard deviations in parentheses.

Assemblage characteristic	Edge N = 13		Platform N = 45		T	P
No. of species	27.8	(3.0)	26.6	(4.0)	444.5	0.259
No. of individuals	285.8	(94.0)	263.2	(120.8)	447.5	0.236
Biomass (g)	19662.2	(24467.9)	6450.9	(5251.4)	551.0	0.002

Additional sampling methods

Large plot sampling for groupers and snappers - Since large commercially-important species are underrepresented in point counts and are best analyzed by frequency of occurrence analysis, we have employed a large plot method on four reefs for 5 years to evaluate the density of snappers and groupers. In 1994, we implemented a visual census method to document the density of groupers and snappers on selected reefs around St. John. Each survey area of 5000 m^2 of reef habitat at four sites is sampled by conducting twenty-five 50x4 m adjacent belt transects. This is accomplished by 4-6 divers conducting adjacent transects from reef edge onto reef platform to 50 m, then moving to adjacent transects until 100 m of reef edge had been surveyed. All groupers and snappers observed by divers are recorded to species and size. Divers move together at the same relative speed to ensure consistency and communication. This allows for avoidance of duplicate counts. The transect swimming rate was standardized so that each transect was conducted within 25-30 min. The four reefs selected for sampling are Haulover reef west, Newfound reef north, Yawzi Point reef, and Tektite reef. This method is a complete census of all individuals observed over a 5000 sq. m. area and does not require sample size estimates. However, it should be evaluated as the most efficient method to obtain densities of these important species. A future sample size project should be conducted to determine if random transects over the same survey area could provide more efficient sampling. The large plot would be valuable comparative data.

Recently recruited fishes – The great majority of tropical reef fishes have planktonic larvae. Since most reef fishes have high site fidelity during their juvenile and adults stages, local reef fish populations must be replenished from the planktonic pool of larvae. Local recruitment is highly variable over space and time and profoundly influences the population dynamics of the adult assemblage structure. In order to examine recruitment variability among dominant habitats around St. John, we conducted juvenile fish recruitment surveys at Yawzi Point Reef, Newfound

Bay, Tektite Reef, Haulover Bay and other locations throughout Greater Lameshur Bay during July 1997 using established methodology. Fish recruits (recently settled post-larval juveniles) were counted along 50 X 2 m strip transects (Fowler et al. 1992). Each diver recorded individual species and size for each recruit encountered along the transect. The transect swimming rate was standardized so that each transect was conducted within 25-30 min. Recruits were defined as observed individuals that had recently settled from the plankton to available substrate, and for most species, were less than or equal to 3 cm TL (total length). Fishes in certain taxa [hamlets (*Hypoplecterus* spp.), butterflyfishes (Chaetodontidae), angelfishes (Pomacanthidae), and surgeonfishes (Acanthuridae)], settle at larger sizes and were recorded at sizes up to 5 cm. Groupers (Serranidae) and snappers (Lutjanidae) also settle at larger sizes and were recorded at sizes less than or equal to 10 cm TL during the survey. Small reef fishes, such as blennies and gobies (particularly the locally abundant masked goby, *Coryphopterus personatus*), reach adult size at 3 cm or less, therefore, recruits for these species were defined as individuals 1 cm or less in size. Monthly sampling of recruits has been conducted at Lameshur Bay for over two years. We propose that a future sample size project be conducted to determine the optimal number of samples required for recently recruited fishes.

Discussion

Management decisions are often based on perceived changes in the sample populations being examined. Resource managers need to know the degree of accuracy associated with population estimates in order to use these data confidently. Detecting a 25% change in mean abundance may be adequate for some species or locations and insufficient for others. The number of samples taken is an important decision in any biological study because of the time and cost involved in data collection. These decisions are often based on practical as well as theoretical considerations.

Our usual sample size of 18 censuses at Tektite Reef appears adequate to detect changes in number of species and number of individuals for the entire assemblage and for many trophic guilds at a 20% level. Even with a complete census of the reef (58 censuses), it would not be possible to detect changes in biomass or number of individuals for some trophic guilds. For some trophic guilds such as herbivores and mobile invertebrate feeders, the current sample design is able to detect changes in number and biomass. Biomass and abundance of large commercially important species (snappers/groupers) are currently sampled using our large plot sample design. This effort represents a single sampling event at one time on one reef. Continued stratification by edge and platform microhabitats seems appropriate based on differences in biomass and DCA results for assemblage structure. These data can be compared to existing point count data for these species. For number of species, number of individuals, and biomass there were no significant differences between values obtained using random vs. haphazard sampling. From these results, continues haphazard sampling appears to be preferable to random sampling due to the time and cost involved in the latter sample design.

Despite high variances associated with abundance and biomass of some trophic guilds and species, repeated sampling over time can detect changes that are useful for management

purposes. Even with coefficients of variation of 100%, our current sampling protocol for Tektite Reef can detect an ongoing decline of 5% in nine years. Increasing alpha levels to 0.20 would improve the ability to detect these changes and is consistent with the precautionary approach to management. It is far better to make a Type I error rather than a Type II error if the sustainability of the resources is in question.

In order to address the issue of number of sites and number of samples at a broader spatial scale, a more intensive sampling effort will need to be conducted on other reefs and at a variety of reef types. Estimates of density from large plot snapper/groupers surveys should be compared to data from point counts conducted on the same reefs to compare these two methods. Determination of the optimal sample design for snapper/grouper surveys and juvenile fish surveys also needs to be conducted. Regardless of the number of sites and samples taken at each site and adopted for monitoring, these results demonstrate differences due to observer bias. These samples were collected by researchers with many years of experience with fish identification, ecological methods, and specifically, fish counting. The bias, error, and variability of samples collected by newly trained and less experienced samplers could be quite large and could lead to problematic time series data. This must be considered in data analysis efforts.

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Appendix I. All fish species (n = 94) observed during the large sampling effort (n = 58) at Tektite Reef. COV = standard deviation/mean. Species are listed in phylogenetic order. Family number from Nelson 1994.

Family number	Family	Genus	Species	COV number	COV biomass
23	Dasyatidae	*Dasyatis*	*americana*	7.62	7.62
43	Elopidae	*Megalops*	*atlanticus*	7.62	7.62
157	Synodontidae	*Synodus*	*intermedius*	2.37	2.88
235	Holocentridae	*Holocentrus*	*adscensionis*	7.62	7.62
235	Holocentridae	*Holocentrus*	*coruscus*	7.62	7.62
235	Holocentridae	*Holocentrus*	*marianus*	3.71	3.79
235	Holocentridae	*Holocentrus*	*rufus*	1.57	1.51
235	Holocentridae	*Myripristis*	*jacobus*	2.05	1.99
254	Aulostomidae	*Aulostomus*	*maculatus*	1.03	1.22
284	Serranidae	*Epinephelus*	*adscensionis*	7.62	7.62
284	Serranidae	*Epinephelus*	*cruentatus*	1.23	1.33
284	Serranidae	*Epinephelus*	*fulvus*	7.62	7.62
284	Serranidae	*Epinephelus*	*guttatus*	1.70	2.11
284	Serranidae	*Epinephelus*	*striatus*	3.28	5.71
284	Serranidae	*Hypoplectrus*	*aberrans*	1.61	1.86
284	Serranidae	*Hypoplectrus*	*chlorurus*	1.90	2.24
284	Serranidae	*Hypoplectrus*	*indigo*	7.62	7.62
284	Serranidae	*Hypoplectrus*	*nigricans*	1.31	1.39
284	Serranidae	*Hypoplectrus*	*puella*	0.64	0.92
284	Serranidae	*Hypoplectrus*	*species*	7.62	7.62
284	Serranidae	*Hypoplectrus*	*unicolor*	2.35	2.46
284	Serranidae	*Mycteroperca*	*interstitialis*	5.34	5.65
284	Serranidae	*Serranus*	*tabacarius*	4.32	6.58
284	Serranidae	*Serranus*	*tigrinus*	5.00	5.00
287	Grammidae	*Gramma*	*loreto*	2.49	2.11
296	Priacanthidae	*Priacanthus*	*cruentatus*	5.34	5.74
306	Carangidae	*Alectis*	*ciliaris*	7.62	7.62
306	Carangidae	*Caranx*	*ruber*	2.02	2.03
316	Lutjanidae	*Lutjanus*	*analis*	7.62	7.62
316	Lutjanidae	*Lutjanus*	*apodus*	2.77	3.17
316	Lutjanidae	*Lutjanus*	*griseus*	2.52	2.63
316	Lutjanidae	*Lutjanus*	*jocu*	7.62	7.62
316	Lutjanidae	*Lutjanus*	*mahogani*	2.26	2.91
316	Lutjanidae	*Lutjanus*	*synagris*	5.26	5.61
316	Lutjanidae	*Ocyurus*	*chrysurus*	2.74	2.68
319	Gerreidae	*Gerres*	*cinereus*	4.96	6.22
320	Haemulidae	*Haemulon*	*aurolineatum*	2.27	2.45
320	Haemulidae	*Haemulon*	*chrysargyreum*	4.63	4.54

Family number	Family	Genus	Species	COV number	COV biomass
320	Haemulidae	*Haemulon*	*flavolineatum*	2.48	1.36
320	Haemulidae	*Haemulon*	*macrostomum*	4.60	4.36
320	Haemulidae	*Haemulon*	*parrai*	6.36	6.61
320	Haemulidae	*Haemulon*	*plumieri*	3.20	3.35
320	Haemulidae	*Haemulon*	*sciurus*	1.50	1.56
321	Inermiidae	*Inermia*	*vitata*	3.44	5.26
322	Sparidae	*Calamus*	*calamus*	3.83	3.99
326	Sciaenidae	*Equetus*	*punctatus*	3.48	3.93
326	Sciaenidae	*Odontoscion*	*dentex*	2.86	3.05
327	Mullidae	*Mulloidichthys*	*martinicus*	2.47	2.50
327	Mullidae	*Pseudupeneus*	*maculatus*	1.45	1.42
338	Chaetodontidae	*Chaetodon*	*capistratus*	1.19	1.24
338	Chaetodontidae	*Chaetodon*	*striatus*	3.94	4.40
339	Chaetodontidae	*Centropyge*	*argi*	3.63	4.00
339	Pomacanthidae	*Holacanthus*	*tricolor*	1.59	1.72
339	Pomacanthidae	*Pomacanthus*	*arcuatus*	7.62	7.62
346	Pomacentridae	*Abudefduf*	*saxatilis*	7.62	7.62
346	Pomacentridae	*Chromis*	*cyanea*	0.78	0.78
346	Pomacentridae	*Chromis*	*multilineatus*	1.16	1.63
346	Pomacentridae	*Microspathodon*	*chrysurus*	1.16	1.32
346	Pomacentridae	*Stegastes*	*diencaeus*	2.18	2.43
346	Pomacentridae	*Stegastes*	*dorsopunicans*	1.98	1.84
346	Pomacentridae	*Stegastes*	*partitus*	0.64	0.74
346	Pomacentridae	*Stegastes*	*planifrons*	0.46	0.63
346	Pomacentridae	*Stegastes*	*variabilis*	0.90	1.04
356	Sphyraenidae	*Sphyraena*	*barracuda*	5.34	6.84
358	Labridae	*Bodianus*	*rufus*	2.46	2.97
358	Labridae	*Clepticus*	*parrai*	3.12	2.51
358	Labridae	*Halichoeres*	*garnoti*	0.71	0.87
358	Labridae	*Halichoeres*	*maculipinna*	1.94	2.36
358	Labridae	*Halichoeres*	*pictus*	2.19	2.03
358	Labridae	*Halichoeres*	*radiatus*	5.34	5.36
358	Labridae	*Thalassoma*	*bifasciatum*	0.83	1.29
360	Scaridae	*Scarus*	*croicensis*	1.01	1.08
360	Scaridae	*Scarus*	*taeniopterus*	2.16	2.04
360	Scaridae	*Scarus*	*vetula*	2.01	2.77
360	Scaridae	*Sparisoma*	*atomarium*	3.92	3.97
360	Scaridae	*Sparisoma*	*aurofrenatum*	0.69	0.86
360	Scaridae	*Sparisoma*	*chrysopterum*	7.62	7.62
360	Scaridae	*Sparisoma*	*rubripinne*	2.91	3.20
360	Scaridae	*Sparisoma*	*viride*	0.90	1.08
375	Opistognathidae	*Opistognathus*	*aurifrons*	4.28	4.35

Family number	Family	Genus	Species	COV number	COV biomass
403	Gobiidae	*Coryphopterus*	*glaucofraenum*	6.25	5.66
403	Gobiidae	*Gobiosoma*	*evelynae*	4.50	4.71
409	Acanthuridae	*Acanthurus*	*bahianus*	4.79	3.47
409	Acanthuridae	*Acanthurus*	*chirurgus*	4.95	3.18
409	Acanthuridae	*Acanthurus*	*coeruleus*	2.05	1.27
414	Scombridae	*Scomberomorus*	*regalis*	3.71	3.81
440	Balistidae	*Balistes*	*vetula*	3.48	3.81
440	Balistidae	*Cantherhinus*	*pullus*	3.28	3.55
440	Balistidae	*Monacanthus*	*tuckeri*	7.62	7.62
441	Ostraciidae	*Lactophrys*	*bicaudalis*	5.34	5.41
441	Ostraciidae	*Lactophrys*	*polygonia*	4.50	4.53
441	Ostraciidae	*Lactophrys*	*triqueter*	2.65	2.82
443	Tetraodontidae	*Canthigaster*	*rostrata*	0.93	1.00
444	Diodontidae	*Diodon*	*holocanthus*	7.62	7.62